

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/572,932  
Source: IFWP  
Date Processed by STIC: 3/31/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 03/31/2006

PATENT APPLICATION: US/10/572,932

TIME: 12:21:49

Input Set : A:\082368-007600US.txt

Output Set: N:\CRF4\03292006\J572932.raw

```

4 <110> APPLICANT: Nakamura, Yusuke
5     Furukawa, Yoichi
7 <120> TITLE OF INVENTION: METHOD FOR DIAGNOSING HEPATOCELLULAR
8     CARCINOMAS
10 <130> FILE REFERENCE: 082368-007600US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/572,932
C--> 12 <141> CURRENT FILING DATE: 2006-03-21
12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/013722
13 <151> PRIOR FILING DATE: 2004-09-14
15 <150> PRIOR APPLICATION NUMBER: US 60/505,632
16 <151> PRIOR FILING DATE: 2003-09-24
18 <160> NUMBER OF SEQ ID NOS: 28
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1528
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (133)...(1308)
31 <400> SEQUENCE: 1
32 ccacgcgtcc gcgggagcgg agccgtggcg cgctcgcccc ggacgccggc cgccccctccg 60
33 ctgcgcctac tgagcgagcg gcccggggcg ccgagggggtc cgcgcgcgcg ggggcgcacc 120
34 gccctggccg cc atg tgc tcc cag ctg tgg ttc ctg acg gac cgg cgc atc 171
35             Met Cys Ser Gln Leu Trp Phe Leu Thr Asp Arg Arg Ile
36             1             5             10
38 cgc gag gac tac ccg cag gtg cag atc ctg cgc gcc ctg cgg cag cgc 219
39 Arg Glu Asp Tyr Pro Gln Val Gln Ile Leu Arg Ala Leu Arg Gln Arg
40             15             20             25
42 tgc tcc gag cag gac gtg cgc ttc cgg gcg gtg ctt atg gac cag atc 267
43 Cys Ser Glu Gln Asp Val Arg Phe Arg Ala Val Leu Met Asp Gln Ile
44             30             35             40             45
46 gcc gtc acc atc gtc ggc ggc cac ctg ggc ctg cag cta aac cag aag 315
47 Ala Val Thr Ile Val Gly Gly His Leu Gly Leu Gln Leu Asn Gln Lys
48             50             55             60
50 gcc ctg acc act ttc ccg gat gtg gtg ctt gta cgg gta ccc aca ccc 363
51 Ala Leu Thr Thr Phe Pro Asp Val Val Leu Val Arg Val Pro Thr Pro
52             65             70             75
54 tca gtg cag tca gac agt gac atc act gtc ctg cga cac ctg gag aag 411
55 Ser Val Gln Ser Asp Ser Asp Ile Thr Val Leu Arg His Leu Glu Lys
56             80             85             90
58 ctg ggc tgc cgg ttg gtc aat cgc cca cag agc atc tta aat tgc atc 459
59 Leu Gly Cys Arg Leu Val Asn Arg Pro Gln Ser Ile Leu Asn Cys Ile

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60	95	100	105	
62	aac aaa ttc tgg acg ttc	caa gaa ctg gct gga cat	ggg gtc ccc atg	507
63	Asn Lys Phe Trp Thr Phe	Gln Glu Leu Ala Gly His	Gly Val Pro Met	
64	110	115	120	125
66	cca gac acc ttc tcc tat	ggt ggg cat gaa gac ttt	tca aaa atg att	555
67	Pro Asp Thr Phe Ser Tyr	Gly Gly His Glu Asp Phe	Ser Lys Met Ile	
69	130	135	140	
71	gat gaa gct gag ccc ctg	ggc tac cca gtc gtg gtg	aag agc aca cga	603
72	Asp Glu Ala Glu Pro Leu	Gly Tyr Pro Val Val Val	Lys Ser Thr Arg	
73	145	150	155	
75	ggc cac cgg gga aaa gct	gtt ttt ctg gca aga gat	aaa cat cac ctc	651
76	Gly His Arg Gly Lys Ala	Val Phe Leu Ala Arg Asp	Lys His His Leu	
77	160	165	170	
79	tct gac atc tgc cat ctg	atc cgc cac gat gtg ccc	tac ctg ttc cag	699
80	Ser Asp Ile Cys His Leu	Ile Arg His Asp Val Pro	Tyr Leu Phe Gln	
81	175	180	185	
83	aag tac gtg aag gag tcc	cat gga aag gac atc cgg	gtg gtg gtg gta	747
84	Lys Tyr Val Lys Glu Ser	His Gly Lys Asp Ile Arg	Val Val Val Val	
85	190	195	200	205
87	ggg ggc cag gtc ata ggc	tct atg ctt cgc tgc tcc	act gat gga cgg	795
88	Gly Gly Gln Val Ile Gly	Ser Met Leu Arg Cys Ser	Thr Asp Gly Arg	
89	210	215	220	
91	atg cag agc aac tgc tct	ctc ggt ggc gtg ggc gtc	aag tgt ccg ctg	843
92	Met Gln Ser Asn Cys Ser	Leu Gly Gly Val Gly Val	Lys Cys Pro Leu	
93	225	230	235	
95	aca gaa caa ggc aag cag	ttg gct att cag gtg tcc	aac atc cta ggc	891
96	Thr Glu Gln Gly Lys Gln	Leu Ala Ile Gln Val Ser	Asn Ile Leu Gly	
97	240	245	250	
99	atg gac ttc tgt ggc att	gat ctc ctt atc atg gac	gat ggc tcc ttt	939
100	Met Asp Phe Cys Gly Ile	Asp Leu Leu Ile Met Asp	Asp Gly Ser Phe	
101	255	260	265	
103	gtg gtg tgt gag gca aat	gct aat gtt ggc ttc cta	gcc ttt gac cag	987
104	Val Val Cys Glu Ala Asn	Ala Asn Val Gly Phe Leu	Ala Phe Asp Gln	
105	270	275	280	285
107	gca tgc aac tta gat gtg	ggt ggg atc att gca gac	tat acc atg tcc	1035
108	Ala Cys Asn Leu Asp Val	Gly Gly Ile Ile Ala Asp	Tyr Thr Met Ser	
109	290	295	300	
111	ttg ctg cca aat agg cag	act gga aag atg gct gtc	ctc cca gga ctg	1083
112	Leu Leu Pro Asn Arg Gln	Thr Gly Lys Met Ala Val	Leu Pro Gly Leu	
113	305	310	315	
115	tcg agt cca agg gag aag	aac gag ccg gat ggc tgt	gct tca gct cag	1131
116	Ser Ser Pro Arg Glu Lys	Asn Glu Pro Asp Gly Cys	Ala Ser Ala Gln	
117	320	325	330	
119	gga gtt gca gag agc gtc	tat acc atc aac agt ggg	tct acc tct agc	1179
120	Gly Val Ala Glu Ser Val	Tyr Thr Ile Asn Ser Gly	Ser Thr Ser Ser	
121	335	340	345	
123	gaa agt gag cct gaa ctg	gga gag atc cgg gat tcc	tca gca agc aca	1227
124	Glu Ser Glu Pro Glu Leu	Gly Glu Ile Arg Asp Ser	Ser Ser Ala Ser Thr	
125	350	355	360	365

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```

127 atg ggg gcc cca ccc tcc atg ctg ccc gaa cct ggc tac aac att aac 1275
128 Met Gly Ala Pro Pro Ser Met Leu Pro Glu Pro Gly Tyr Asn Ile Asn
129          370          375          380
131 aac agg att gct tct gag tta aaa ctt aag tga attcctgctt tttggcagca 1328
132 Asn Arg Ile Ala Ser Glu Leu Lys Leu Lys
133          385          390
135 tttaaacc aa atcctactgc ttccctagta gttttgagtg aataaaatct ggactaatgt 1388
136 gatttcattt gcacagaaac tagaaatccc atctgggcac tcagcatttt ttctaacgat 1448
137 gatttaagca aatggcctag ctttgtgggtt ttacaaaaga caaatataaa aacactcaca 1508
138 agaacaaaaa aaaaaaaaaa 1528
140 <210> SEQ ID NO: 2
141 <211> LENGTH: 391
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
145 <400> SEQUENCE: 2
146 Met Cys Ser Gln Leu Trp Phe Leu Thr Asp Arg Arg Ile Arg Glu Asp
147 1          5          10          15
148 Tyr Pro Gln Val Gln Ile Leu Arg Ala Leu Arg Gln Arg Cys Ser Glu
149          20          25          30
150 Gln Asp Val Arg Phe Arg Ala Val Leu Met Asp Gln Ile Ala Val Thr
151          35          40          45
152 Ile Val Gly Gly His Leu Gly Leu Gln Leu Asn Gln Lys Ala Leu Thr
153          50          55          60
154 Thr Phe Pro Asp Val Val Leu Val Arg Val Pro Thr Pro Ser Val Gln
155 65          70          75          80
156 Ser Asp Ser Asp Ile Thr Val Leu Arg His Leu Glu Lys Leu Gly Cys
157          85          90          95
158 Arg Leu Val Asn Arg Pro Gln Ser Ile Leu Asn Cys Ile Asn Lys Phe
159          100         105         110
160 Trp Thr Phe Gln Glu Leu Ala Gly His Gly Val Pro Met Pro Asp Thr
161          115         120         125
162 Phe Ser Tyr Gly Gly His Glu Asp Phe Ser Lys Met Ile Asp Glu Ala
163          130         135         140
164 Glu Pro Leu Gly Tyr Pro Val Val Val Lys Ser Thr Arg Gly His Arg
165 145         150         155         160
166 Gly Lys Ala Val Phe Leu Ala Arg Asp Lys His His Leu Ser Asp Ile
167          165         170         175
168 Cys His Leu Ile Arg His Asp Val Pro Tyr Leu Phe Gln Lys Tyr Val
169          180         185         190
170 Lys Glu Ser His Gly Lys Asp Ile Arg Val Val Val Val Gly Gly Gln
171          195         200         205
172 Val Ile Gly Ser Met Leu Arg Cys Ser Thr Asp Gly Arg Met Gln Ser
173          210         215         220
174 Asn Cys Ser Leu Gly Gly Val Gly Val Lys Cys Pro Leu Thr Glu Gln
175 225         230         235         240
176 Gly Lys Gln Leu Ala Ile Gln Val Ser Asn Ile Leu Gly Met Asp Phe
177          245         250         255
178 Cys Gly Ile Asp Leu Leu Ile Met Asp Gly Ser Phe Val Val Cys
179          260         265         270

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180 Glu Ala Asn Ala Asn Val Gly Phe Leu Ala Phe Asp Gln Ala Cys Asn
181      275      280      285
182 Leu Asp Val Gly Gly Ile Ile Ala Asp Tyr Thr Met Ser Leu Leu Pro
183      290      295      300
184 Asn Arg Gln Thr Gly Lys Met Ala Val Leu Pro Gly Leu Ser Ser Pro
185 305      310      315      320
186 Arg Glu Lys Asn Glu Pro Asp Gly Cys Ala Ser Ala Gln Gly Val Ala
187      325      330      335
188 Glu Ser Val Tyr Thr Ile Asn Ser Gly Ser Thr Ser Ser Glu Ser Glu
189      340      345      350
191 Pro Glu Leu Gly Glu Ile Arg Asp Ser Ser Ala Ser Thr Met Gly Ala
192      355      360      365
193 Pro Pro Ser Met Leu Pro Glu Pro Gly Tyr Asn Ile Asn Asn Arg Ile
194      370      375      380
195 Ala Ser Glu Leu Lys Leu Lys
196 385      390
199 <210> SEQ ID NO: 3
200 <211> LENGTH: 22
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
206 RT-PCR
208 <400> SEQUENCE: 3
209 acaacagcct caagatcatc ag 22
211 <210> SEQ ID NO: 4
212 <211> LENGTH: 20
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
218 RT-PCR
220 <400> SEQUENCE: 4
221 ggtccaccac tgacacgttg 20
223 <210> SEQ ID NO: 5
224 <211> LENGTH: 23
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
230 RT-PCR
232 <400> SEQUENCE: 5
233 caaataggca gactggaaag atg 23
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 23
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: An artificially synthesized primer sequence for

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TIME: 12:21:49

Input Set : A:\082368-007600US.txt

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```

242      RT-PCR
244 <400> SEQUENCE: 6
245 ctagggaagc agtaggattt ggt                                23
247 <210> SEQ ID NO: 7
248 <211> LENGTH: 30
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
254      RT-PCR
256 <400> SEQUENCE: 7
257 attgtcgacg ctgcccctac tgagcgagcg                            30
259 <210> SEQ ID NO: 8
260 <211> LENGTH: 36
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
266      RT-PCR
268 <400> SEQUENCE: 8
269 aatctcgaga gcaggaattc acttaagttt taactc                      36
271 <210> SEQ ID NO: 9
272 <211> LENGTH: 22
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
278      RT-PCR
280 <400> SEQUENCE: 9
281 tggtagccaa gtgcaggтта ta                                    22
283 <210> SEQ ID NO: 10
284 <211> LENGTH: 22
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
290      RT-PCR
292 <400> SEQUENCE: 10
293 ccaaagggtt tctgcagttt ca                                    22
295 <210> SEQ ID NO: 11
296 <211> LENGTH: 30
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: An artificially synthesized primer sequence for
302      RT-PCR
304 <400> SEQUENCE: 11
305 tgcggatcca gagcagattg tactgagagt                            30
307 <210> SEQ ID NO: 12

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**VERIFICATION SUMMARY**

PATENT APPLICATION: **US/10/572,932**

DATE: 03/31/2006

TIME: 12:21:50

Input Set : **A:\082368-007600US.txt**

Output Set: **N:\CRF4\03292006\J572932.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date